

Figure 1

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCCGGCAGCTCTATTGCCGACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCACGGCAGCGTCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAACCTCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCACTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

```
Query:      170 TGGCGCACCTGCACGGCATCCTGCGCCGCCGGCAGTCTATTGCCGCACC GGCTTC CACC   229
                ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct:       2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTC ACT    61

Query:     230 TGCAGATCCTGCCCCGACGGCAGCGTG CAGGGCACCCGGCAGGACCACAGCCTCTTCCGT A   289
                ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct:     62 TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATT TGCA   121

Query:     290 TCTTGAATTTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC   349
                ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct:    122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATT CGAGGCGTGGACAGTGGAC   181

Query:     350 TCTATCTTGGAATGAATGACA AAGGAGA ACTCTATGGATCAGAGAACTTACTTCCGAAT   409
                |||| | | | | | | | | | | | | | | | | | | | |
Sbjct:    182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT   241

Query:     410 GCATCTTTAGGGAGCAGTTTGAAGAGA ACTGGTATAACACCTATT CATCTAACATATATA   469
                || | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    242 GTGTATT CAGAGAACAGTT CGAAGAAA CTGGTATA ATACGTACTCGTCAAACCTATATA   301

Query:     470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGA ACTCCAAGAG   529
                || | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    302 AGCACGTGGACACTGGAAGGC GATACTATGTTGCATT AAATAAAGATGGGACCCCGAGAG   361

Query:     530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC   589
                || | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC   421


Query:     590 CAGA 593
                |||
Sbjct:     422 CCGA 425
```

Figure 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%), Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCTCGCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTCGCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||
Sbjct: 15987 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGGCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 110
          |||
Sbjct: 16046 GCTGCGCAGCCCCCGGCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGGCGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
          |||
Sbjct: 16106 GCAGCGGCGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query:    49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
          |||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%), Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCTTGTACAATTCTGGAACCTTTCTGGATCCACTGGTCTAGG 574
          |||
Sbjct: 7257 AGTGATACATCAGTAGGTCTTGTACAATTCTGGAACCTTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 514
          |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 7376

Query:   513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACCAGTTCTCTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
          |||
Sbjct: 7437 ATAGGTGTTATACCAGTTCTCTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496

Query:   393 CTC-TGATCCATAGA 380
          |||
Sbjct: 7497 CTCCTGAAAGAGAGA 7511
```

Figure 3 (cont.)

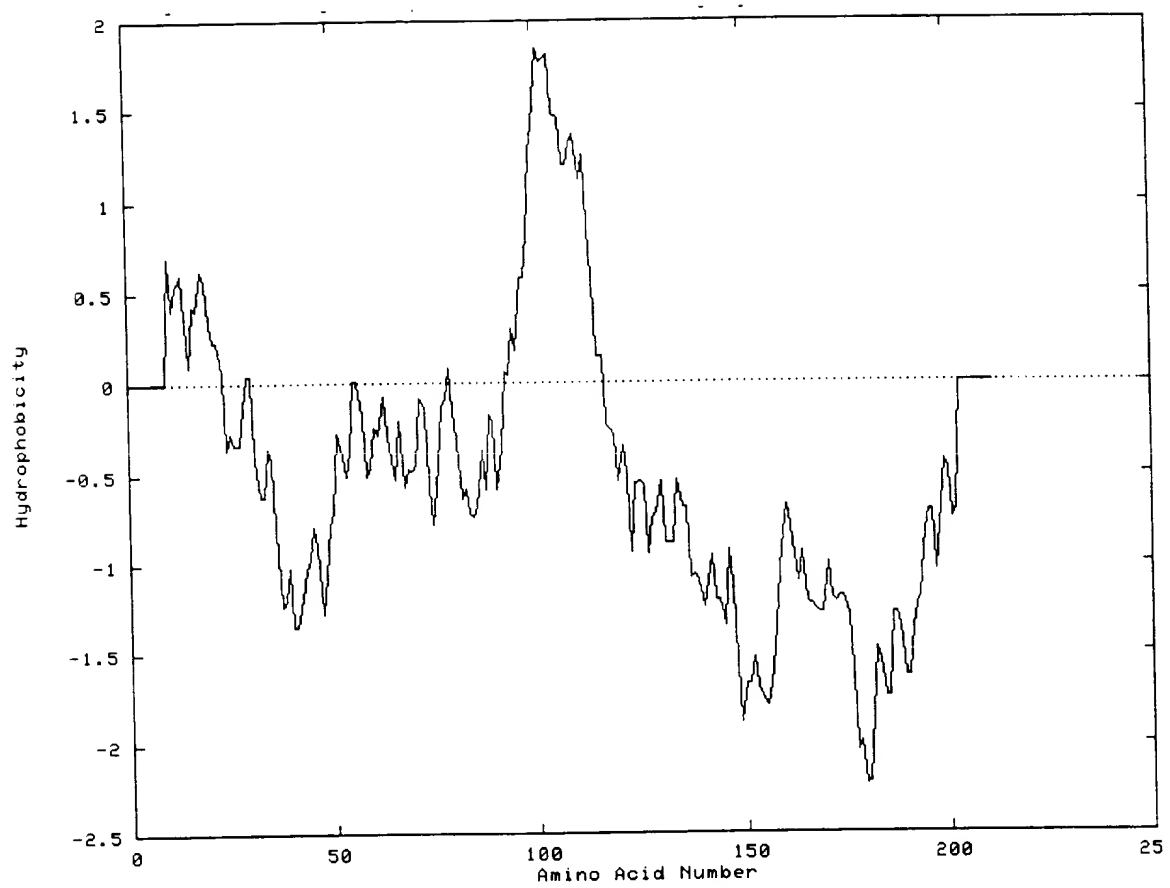
C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 106/106 (100%), Positives = 106/106 (100%), Strand = Minus / Plus

```
Query:   391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCTCAAGATAGAGACCACTGTCCACACCTC 332
          |||
Sbjct:  9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCTCAAGATAGAGACCACTGTCCACACCTC 9896

Query:   331 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 286
          |||
Sbjct:  9897 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 9942
```

Figure 4



ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

```

Query:      1  MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH  59
           |||| ||| + | + + | + +|| + | || + +| || | |
Sbjct:      1  MAPLGEVGNFYFGVQDAV--PFGNVPLVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH  56

Query:      60  LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLSFGILEFISVAVGLVSIKRGVDSGLYL  119
           | ||||| ||||| ||||| +| | +| +| ||| +| ||||| +| |||||
Sbjct:      57  LKGILRRRQLYCRTGFHLEIFPNGTIQGRKDHRSFGILEFISIAVGLVSIKRGVDSGLYL  116

Query:      120  GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTTPRDA  179
           ||| +| ||||| ||||| ||| +| ||||| ||||| ||||| +| ||||| +|
Sbjct:      117  GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTTPREGT  176

Query:      180  RSKRHQKFTHFLRPVDPERVPELYKDIL  208
           | +| ||||| ||||| ||||| ||| +| ||||| ||||| +|
Sbjct:      177  RTKRHQKFTHFLRPVDPDKVPELYKDIL  205

```

Figure 6

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76

Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
             |||| ||| + | + + | + +|| + | || + +| || ||
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLGILEFISVAVGLVSIRGVDSGLYL 119
             | ||||| ||||| ||||| +| |+|++||| +||| ||||| ||| +||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
             ||| +||| ||||| ||| +||| ||||| ||||| ||| +||| ||||| ||||| +|
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
             |+||| ||||| ||||| ||| ++||| ||| +|
Sbjct:    177 RTKRHQKFTHFLPRPVDPAKVPVLYKDIL 205
```

Figure 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76

Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
            |||| ||| + | + + | + +|| + | || + +| || ||
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLFGILEFISVAVGLVSIRGVDSGLYL 119
            | ||||| ||||| ||||| +| | +| +| ||| ||||| ||||| +| ||||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
            ||| +| ||||| ||||| || +| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
            | +| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    177 RTKRHQKFTHFLPRPVDPAKVPPELYKDIL 205
```


Figure 8

FGF-CX Query Length = 211
XFGF-20 Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
             |||||+|| |||| + ||| ||||| ||||| + | | + + +|| +| | + |||
Sbjct:      1 MAPLADVGTFLGGYDALGQ-VGSHFLLPPAKDSPLLFNDPLAQSERLSRSAP--SDLSHL 57

Query:     61 HGILRRRQLYCRTGFHLQILPDGVSQGTRQDHSFLFGILEFISVAVGLVSIRGVDSGLYLG 120
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     58 QGILRRRQLYCRTGFHLQILPDGNVQGTRQDHSRFGILEFISVAIGLVSIRGVDTGLYLG 117

Query:    121 MNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    118 MNDKGELFGSEKLTSECFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGTR 177

Query:    181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
             +||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    178 AKRHQKFTHFLPRPVDPEKVPELYKDLMGYS 208
```

FIGURE 9

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-20 (BAA83474Xen; Xenopus laevis XFGF-20) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

| | |
|-----------------|---|
| HUMAN FGF-9 | M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H |
| RAT FGF-9 | M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H |
| MOUSE FGF-9 | M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H |
| XENOPUS XFGF-20 | M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S A P - - S D L S H |
| FGF-CX | M A P L A E V G G F L G L E G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A A E R S A R - G G P G A A Q L A H |
| HUMAN FGF-9 | L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L |
| RAT FGF-9 | L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L |
| MOUSE FGF-9 | L K G I L R R R R Q L Y C R T G T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L |
| XENOPUS XFGF-20 | L Q G I L R R R R Q L Y C R T G T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S V A I G L V S I R G V D T G L Y L |
| FGF-CX | L H G I L R R R R Q L Y C R T G T G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L |
| HUMAN FGF-9 | G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T |
| RAT FGF-9 | G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T |
| MOUSE FGF-9 | G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R R Y Y V A L N K D G T P R E G T |
| XENOPUS XFGF-20 | G M N D K G E L F G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R R Y F V A L N K D G T P R D G T |
| FGF-CX | G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N I Y K H G D T G R R R Y F V A L N K D G T P R D G A |
| HUMAN FGF-9 | R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S |
| RAT FGF-9 | R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S |
| MOUSE FGF-9 | R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S |
| XENOPUS XFGF-20 | R A K R H Q K F T H F L P R P V D P E K V P E L Y K D L M G Y S |
| FGF-CX | R S K R H Q K F T H F L P R P V D P E R V P E L Y K D L L M Y T |